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<120> Plant Lecithin:Cholesterol Acyltransferases  
<130> BB1262  
<140> US/09/857,612  
<141> 2001-07-19  
<150> 60/110,782  
<151> 1998-12-03  
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<213> Zea mays  
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<223> n=A, C, G, or T

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<210> 2

<211> 143

<212> PRT

<213> Zea mays

<400> 2

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Val Ala His Ser Tyr Gly Gly Thr Leu Ala His Gln Phe Leu Leu Arg
  1           5           10           15

Arg Pro Leu Pro Trp Arg Arg Arg Phe Val Arg Arg Phe Val Pro Val
      20           25           30

Ala Ala Pro Trp Gly Gly Val Val Leu Gly Met Leu Thr Ile Val Ala
      35           40           45

Gly Asn Asn Leu Gly Leu Pro Phe Val Asp Pro Leu Ala Leu Lys Gly
      50           55           60

Glu Tyr Arg Ser Leu Gln Ser Ser Leu Trp Pro Leu Pro Asn Pro Asn
      65           70           75           80

Ala Phe Arg Ala Gly Gln Pro Leu Val Thr Thr Arg Ser Arg Thr Tyr
      85           90           95

Thr Ala His Asp Met Ala Asp Phe Leu Asp Ala Ile Gly Leu Gly Ala
      100          105          110

Ala Ile Val Pro Tyr Gln Ser Arg Val Leu Pro Leu Phe Arg Glu Leu
      115          120          125

Pro Ser Pro Arg Val Pro Val Ala Cys Val Arg Pro Gly Leu Gly
      130          135          140
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<211> 921

<212> DNA

<213> Zea mays

<220>

<221> unsure

<222> (884)

<223> n=A, C, G, or T

<400> 3

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<210> 4  
 <211> 233  
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 <213> Zea mays

<400> 4

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Met Ala Ser Ser Leu Leu Gln Gln Leu Leu Ser Leu Leu Leu Leu Leu
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Leu Pro Ser Pro Leu Arg Leu Arg Glu His Leu Ser Gly Asn His Ala
      20                      25                      30

Val Ser Ala Asn Asn Phe His Pro Ile Phe Leu Val Ala Gly Val Ser
      35                      40                      45

Cys Ser Asp Leu Glu Ala Arg Leu Thr Glu Glu Tyr Arg Pro Ser Val
      50                      55                      60

Pro His Cys Gly Ala Met Lys Gly Lys Gly Trp Phe Gly Leu Trp Lys
      65                      70                      75                      80

Asn Ser Ser Glu Leu Leu Ser Arg Asp Tyr Val Gln Cys Phe Glu Glu
      85                      90                      95

Gln Met Ser Leu Val Tyr Asp Pro Ala Ile Asn Glu Tyr Arg Asn Leu
      100                      105                      110

Ala Gly Val Glu Thr Arg Val Pro Asn Phe Gly Ser Thr Arg Ala Phe
      115                      120                      125

Ser His Lys Asn Pro Leu Lys Ser Asp Trp Cys Leu Gly Lys Leu Arg
      130                      135                      140

Ala Ala Leu Glu Asp Met Gly Tyr Arg Asp Gly Asp Thr Met Phe Gly
      145                      150                      155                      160

Ala Pro Tyr Asp Phe Arg Tyr Ala Pro Pro Ser Pro Gly Gln Thr Ser
      165                      170                      175

Glu Val Tyr Ser Arg Tyr Phe Lys Glu Leu Met Glu Leu Val Glu Ala
      180                      185                      190

Ala Ser Glu Arg Thr Arg Lys Lys Ala Val Ile Leu Gly His Ser Phe
      195                      200                      205

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Gly Gly Met Val Ala Leu Glu Phe Val Arg Asn Thr Pro Pro Ala Trp  
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Arg Arg Glu His Ile Glu Arg Leu Val  
 225 230

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 <211> 1217  
 <212> DNA  
 <213> Glycine max

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 ttcattacca ccaagaactc gatgattact tcaacactcc tgggggttgag acccgggtcc 180  
 ctcaactttg ttccaccaac tctcttctct atctcaatcc tcgtctcaag catatcaccg 240  
 gatacatggc acccctggta gattcattac aaaagcttgg ctacgctgat ggtgagactc 300  
 tgtttggagc cccttatgac tttagatatg gtctagctgc tgaaggtcac ccttcacaag 360  
 tgggtttcaa gttcctcaaa gatctaaaga atttgataga agaagcaagc aattccaata 420  
 atgggaagcc agtgatactt ctctcccaca gtttaggagg cctatttgtc ctacaactac 480  
 taaatagaaa cccccctct tggcgcaaaa aattcatcaa acacttcatt gctctttcag 540  
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 ggcttttgcc taacccaaaa atttttggtc ctcaaaaacc aatagtata actccaatta 720  
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 tttatcctta tgaaacacga attctaccct tgatagggaa cataaaaagca ccacaagtgc 840  
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 <211> 381  
 <212> PRT  
 <213> Glycine max

<400> 6  
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 20 25 30  
 Cys Phe Ala Glu Arg Met Thr Leu His Tyr His Gln Glu Leu Asp Asp  
 35 40 45  
 Tyr Phe Asn Thr Pro Gly Val Glu Thr Arg Val Pro His Phe Gly Ser  
 50 55 60  
 Thr Asn Ser Leu Leu Tyr Leu Asn Pro Arg Leu Lys His Ile Thr Gly  
 65 70 75 80  
 Tyr Met Ala Pro Leu Val Asp Ser Leu Gln Lys Leu Gly Tyr Ala Asp  
 85 90 95  
 Gly Glu Thr Leu Phe Gly Ala Pro Tyr Asp Phe Arg Tyr Gly Leu Ala

100	105	110
Ala Glu Gly His Pro Ser Gln Val Gly Ser Lys Phe Leu Lys Asp Leu		
115	120	125
Lys Asn Leu Ile Glu Glu Ala Ser Asn Ser Asn Asn Gly Lys Pro Val		
130	135	140
Ile Leu Leu Ser His Ser Leu Gly Gly Leu Phe Val Leu Gln Leu Leu		
145	150	155
Asn Arg Asn Pro Pro Ser Trp Arg Lys Lys Phe Ile Lys His Phe Ile		
165	170	175
Ala Leu Ser Ala Pro Trp Gly Gly Ala Ile Asp Glu Met Tyr Thr Phe		
180	185	190
Ala Ser Gly Asn Thr Leu Gly Val Pro Leu Val Asp Pro Leu Leu Val		
195	200	205
Arg Asp Glu Gln Arg Ser Ser Glu Ser Asn Leu Trp Leu Leu Pro Asn		
210	215	220
Pro Lys Ile Phe Gly Pro Gln Lys Pro Ile Val Ile Thr Pro Ile Arg		
225	230	235
Pro Tyr Ser Ala His Asp Met Val Asp Phe Leu Lys Asp Ile Gly Phe		
245	250	255
Pro Glu Gly Val Tyr Pro Tyr Glu Thr Arg Ile Leu Pro Leu Ile Gly		
260	265	270
Asn Ile Lys Ala Pro Gln Val Pro Ile Thr Cys Ile Met Gly Thr Gly		
275	280	285
Val Gly Thr Leu Glu Thr Leu Phe Tyr Gly Lys Gly Asp Phe Asp Glu		
290	295	300
Arg Pro Glu Ile Ser Tyr Gly Asp Gly Asp Gly Thr Val Asn Leu Val		
305	310	315
Ser Leu Leu Ala Leu Gln Ser Leu Trp Lys Glu Glu Lys Asn Gln Tyr		
325	330	335
Leu Lys Val Val Lys Ile Asp Gly Val Ser His Thr Ser Ile Leu Lys		
340	345	350
Asp Glu Val Ala Leu Asn Glu Ile Val Gly Glu Ile Thr Ser Ile Asn		
355	360	365
Ser His Ala Glu Leu Gly Leu Ser Asn Leu Phe Ser Gly		
370	375	380
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<211> 1440		
<212> DNA		
<213> Zea mays		
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gcgtggagt tcgtccggag cactcccatt gcgtggcgag acaggtacat caagcacctc 720
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<210> 8  
 <211> 434  
 <212> PRT  
 <213> Zea mays

<400> 8

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Met Ala Arg Ile Pro Gln Val Leu Ala Pro Leu Leu Leu Leu Leu Leu
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Pro Ala Gly Leu Arg Glu Leu Met Ile Asp Arg Arg Pro Leu Pro Lys
          20             25             30

Arg Cys Arg Arg Glu Val Leu Leu His Pro Leu Val Leu Val Pro Gly
          35             40             45

Leu Thr Cys Ser Glu Leu Asp Ala Arg Leu Thr Asp Ala Tyr Arg Pro
          50             55             60

Phe Arg Ala Ala Cys Asp Glu Gly Glu Gly Leu Val Arg Leu Trp Thr
          65             70             75             80

Asn Cys Ser Asp Leu Pro Ala His His Tyr Val Arg Cys Phe Met Glu
          85             90             95

Gln Met Ala Leu Val Tyr Asp Pro Val Ala Asn Asp Tyr Arg Asn Leu
          100            105            110

Pro Gly Val Glu Thr Arg Val Arg Asn Phe Gly Ser Ser Arg Gly Phe
          115            120            125

Gln Lys Asn Pro Glu His Thr Thr Trp Ser Trp Cys Phe Glu Val Leu
          130            135            140

Arg Asn Glu Leu Ala Arg Ala Gly Tyr Arg Asp Gly Asp Thr Leu Phe
          145            150            155            160

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Gly Ala Pro Tyr Asp Leu Arg Tyr Ala Pro Pro Val Pro Gly Gln Pro  
 165 170 175  
 Ser Arg Ser Ser Pro Ala Thr Ser Val Gly Trp Pro Ser Leu Val Glu  
 180 185 190  
 Asp Ala Ser Arg Lys Asn Arg Gly Arg Lys Val Ile Leu Phe Gly His  
 195 200 205  
 Ser Phe Gly Gly Met Val Ala Leu Glu Phe Val Arg Ser Thr Pro Met  
 210 215 220  
 Ala Trp Arg Asp Arg Tyr Ile Lys His Leu Phe Leu Val Ala Pro Val  
 225 230 235 240  
 Pro Ala Glu Gly Phe Val Lys Pro Leu Gln Tyr Phe Val Ser Gly Ser  
 245 250 255  
 Asn Leu Met Tyr Val Pro Thr Val Ser Ser Leu Glu Pro Ala Phe Arg  
 260 265 270  
 Pro Met Trp Arg Thr Phe Glu Ser Ser Leu Val Asn Phe Pro Ser Pro  
 275 280 285  
 Ala Val Phe Gly Arg Arg Pro Leu Val Val Thr Ala Arg Arg Asn Tyr  
 290 295 300  
 Ser Ala Tyr Asp Leu Glu Asp Leu Leu Val Ala Val Gly Tyr Gly Ala  
 305 310 315 320  
 Gly Val Glu Pro Phe Arg Arg Arg Ala Val Pro Lys Met Ser Tyr Phe  
 325 330 335  
 Gln Ala Pro Met Val Pro Thr Thr Cys Met Asn Gly Val Gly Asn Asp  
 340 345 350  
 Thr Pro Glu Gln Leu Val Tyr Trp Asp Gly Asp Phe Asp Ala Thr Pro  
 355 360 365  
 Glu Ile Val Tyr Gly Asp Gly Asp Asn Ser Ile Asn Leu Val Ser Met  
 370 375 380  
 Leu Ala Phe Asp Glu Lys Met Arg Arg Gln Pro Glu Gln Asn Lys Val  
 385 390 395 400  
 Tyr Lys Ser Ile Lys Ile Arg Gly Ala Gln His Gly Thr Ile Val Thr  
 405 410 415  
 Asp Asp Thr Ala Leu Lys Arg Val Met His Glu Ile Leu Glu Ala Asn  
 420 425 430

Arg Ser

<210> 9  
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 <212> DNA  
 <213> Zea mays

<220>

<221> unsure  
 <222> (536)  
 <223> n=A, C, G, or T

<400> 9

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<210> 10  
 <211> 417  
 <212> PRT  
 <213> Zea mays

<400> 10

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Met Val His Asp Met Ala Ser Cys Ser Arg Gly Gly Thr Ile Val Leu
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Ser Lys Phe Ala Ser Thr Thr Arg Arg Ala Pro Lys Gln Leu Pro Pro
          20             25             30

Val Val Val Val Pro Gly Tyr Ala Thr Asn Glu Leu Asp Ala Arg Leu
          35             40             45

Thr Glu Leu Tyr His Pro Ser Ser Pro Arg Cys Ala His Lys Gly Lys
 50             55             60

Gly Trp Phe Arg Leu Tyr Leu Asn Tyr Thr Ala Leu Glu Asp Ala Ala
 65             70             75             80

Asp Val Arg Cys Phe Ala Glu Gln Met Ala Thr Ala Tyr Asp Ala Ala
          85             90             95

Ser Asp Asp Tyr Arg Asn Ala Gln Gly Val Glu Thr Arg Val Pro Phe
100             105             110

Phe Gly Ser Thr Arg Ala Phe Arg Tyr Pro Asp Pro Asp Arg Arg Asn
115             120             125

```



Phe Ser Tyr Met Asp Lys Phe Val Ser Arg Leu Glu Arg Leu Ala Tyr  
 130 135 140  
 Arg Asp Gly Glu Asn Leu Phe Gly Ala Pro Tyr Asp Phe Arg Tyr Ala  
 145 150 155 160  
 Val Ala Pro Pro Gly His Pro Ser Arg Val Ala Asp Ala Phe Phe Gly  
 165 170 175  
 Arg Leu Arg Arg Leu Val Glu Arg Ala Ser Arg Ala Asn Gly Gly Gly  
 180 185 190  
 Pro Val Thr Ile Val Ala His Ser Tyr Gly Gly Thr Val Ala His Gln  
 195 200 205  
 Phe Leu Leu Arg Arg Pro Leu Pro Trp Arg Arg Arg Phe Val Arg Arg  
 210 215 220  
 Phe Val Pro Val Ala Ala Pro Trp Gly Gly Val Val Leu Gly Met Leu  
 225 230 235 240  
 Thr Ile Val Ala Gly Asn Asn Leu Gly Leu Pro Phe Val Asp Pro Leu  
 245 250 255  
 Ala Leu Lys Gly Glu Tyr Arg Ser Leu Gln Ser Ser Leu Trp Pro Leu  
 260 265 270  
 Pro Asn Pro Asn Ala Phe Arg Ala Gly Gln Pro Leu Val Thr Thr Arg  
 275 280 285  
 Ser Arg Thr Tyr Thr Ala His Asp Met Ala Asp Phe Leu Asp Ala Ile  
 290 295 300  
 Gly Leu Gly Ala Ala Ile Val Pro Tyr Gln Ser Arg Val Leu Pro Leu  
 305 310 315 320  
 Phe Arg Glu Leu Pro Ser Pro Arg Val Pro Val Ala Cys Val Val Gly  
 325 330 335  
 Val Gly Leu Asp Thr Pro Glu Met Leu Ala Tyr Pro Gly Asp Asp Phe  
 340 345 350  
 Asp Val Thr Pro Met Met Val Met Gly Asp Gly Asp Gly Leu Val Asn  
 355 360 365  
 Leu Val Ser Leu Leu Ala Val Asp Pro Ala Trp Arg Leu Pro Thr Ala  
 370 375 380  
 Tyr Phe Arg Met Leu Lys Val Arg Asn Val Ser His Thr Gly Leu Phe  
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 Val Asp Asp Ala Ala Leu Ala Val Ile Ile Ser Ala Ile Leu Arg Pro  
 405 410 415

Asn

<210> 11  
 <211> 1660

<212> DNA  
 <213> Zea mays

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 gagcgccatc gtgaacttcc cgtcgccggc cgtgttcggg cgctgcagg ccgccgtcgt 960  
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 ccgagatggc aagatcaatt tgatcagcgt cttggcgttt gagaaggaga tgcgtcggca 1260  
 gccggagcag aagaagcagt tcaaattccat caagatcaat aaggcccagc attctacgat 1320  
 cgtcacggat gattttgcc tgcacagggt cattcaagaa attgttgagg ccaataatca 1380  
 gaagattcca tcctaaatta ttcattgcat gtatgcatta ccgagctgtg ggggccaata 1440  
 gtgggttggg aagtgatggt ttagacatcg gtcgtggtgt ggtcgcaatt caatcgatta 1500  
 gttatttgtt aacgtcaatt gcttgccctc tgaacttgct gtgataagga aagaccacaa 1560  
 ttattttccg cttgtcgtgt gcgttgatc gtataatgtt aataaaaaa agagtaaaat 1620  
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<210> 12  
 <211> 439  
 <212> PRT  
 <213> Zea mays

<400> 12  
 Met Ala Ser Ser Leu Leu Gln Gln Leu Leu Ser Leu Leu Leu Leu Leu  
 1 5 10 15  
 Leu Pro Ser Pro Leu Arg Leu Arg Glu His Leu Ser Gly Asn His Ala  
 20 25 30  
 Val Ser Ala Asn Asn Phe His Pro Ile Phe Leu Val Ala Gly Val Ser  
 35 40 45  
 Cys Ser Asp Leu Glu Ala Arg Leu Thr Glu Glu Tyr Arg Pro Ser Val  
 50 55 60  
 Pro His Cys Gly Ala Met Lys Gly Lys Gly Trp Phe Gly Leu Trp Lys  
 65 70 75 80  
 Asn Ser Ser Glu Leu Leu Ser Arg Asp Tyr Val Gln Cys Phe Glu Glu  
 85 90 95  
 Gln Met Ser Leu Val Tyr Asp Pro Ala Ile Asn Glu Tyr Arg Asn Leu  
 100 105 110

Ala Gly Val Glu Thr Arg Val Pro Asn Phe Gly Ser Thr Arg Ala Phe  
 115 120 125  
 Ser His Lys Asn Pro Leu Lys Ser Asp Trp Cys Leu Gly Lys Leu Arg  
 130 135 140  
 Ala Ala Leu Glu Asp Met Gly Tyr Arg Asp Gly Asp Thr Met Phe Gly  
 145 150 155 160  
 Ala Pro Tyr Asp Phe Arg Tyr Ala Pro Pro Ser Pro Gly Gln Thr Ser  
 165 170 175  
 Glu Val Tyr Ser Arg Tyr Phe Lys Glu Leu Met Glu Leu Val Glu Ala  
 180 185 190  
 Ala Ser Glu Arg Thr Arg Lys Lys Ala Val Ile Leu Gly His Ser Phe  
 195 200 205  
 Gly Gly Met Val Ala Leu Glu Phe Val Arg Asn Thr Pro Pro Ala Trp  
 210 215 220  
 Arg Arg Glu His Ile Glu Arg Leu Val Leu Val Ala Pro Thr Leu Pro  
 225 230 235 240  
 Gly Gly Phe Leu Glu Pro Val Arg Asn Phe Ala Ser Gly Thr Asp Ile  
 245 250 255  
 Leu Tyr Val Pro Ala Thr Thr Pro Leu Ala Thr Arg Ala Met Trp Arg  
 260 265 270  
 Ser Phe Glu Ser Ala Ile Val Asn Phe Pro Ser Pro Ala Val Phe Gly  
 275 280 285  
 Arg Leu Gln Ala Pro Leu Val Val Thr Arg Glu Arg Asn Tyr Ser Ala  
 290 295 300  
 Ser Ala His Asp Met Glu Arg Phe Leu Ala Ala Val Gly Ser Gly Glu  
 305 310 315 320  
 Ala Ala Glu Pro Phe Arg Arg Arg Ala Val Pro Lys Met Gly Ser Phe  
 325 330 335  
 Ala Ala Pro Met Val Pro Met Thr Tyr Ile Ser Gly Val Gly Asn Arg  
 340 345 350  
 Thr Pro Leu Arg Leu Val Phe Trp Gly Glu Asp Phe Asp Ala Ala Pro  
 355 360 365  
 Glu Val Ala Ala Tyr Gly Asp Arg Asp Gly Lys Ile Asn Leu Ile Ser  
 370 375 380  
 Val Leu Ala Phe Glu Lys Glu Met Arg Arg Gln Pro Glu Gln Lys Lys  
 385 390 395 400  
 Gln Phe Lys Ser Ile Lys Ile Asn Lys Ala Gln His Ser Thr Ile Val  
 405 410 415  
 Thr Asp Asp Phe Ala Leu His Arg Val Ile Gln Glu Ile Val Glu Ala  
 420 425 430

Asn Asn Gln Lys Ile Pro Ser  
435

<210> 13  
<211> 1332  
<212> DNA  
<213> Glycine max

<400> 13  
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gttggttgta tgctgtcatt gctatgcaca tgtggggcaa gcaacctcga ccctttgatt 120  
ctaataaccag gtaacggagg gaaccaacta gaagcaaggt tgaccaatca gtacaagccc 180  
tctactttca tctgcgaatc atggtaccct ctcatacaaga aaaagaatgg atggttcaga 240  
ctttggtttg attccagtgt catacttgct cctttcactc aatgctttgc cgaacgcatg 300  
acccttcatt accaccaaga actcgatgat tacttcaaca ctccctgggt tgagaccggg 360  
gtccctcact ttggttccac caactctctt ctctatctca atcctcgtct caagcatatc 420  
accggataca tggcaccctt ggtagattca ttacaaaagc ttggctacgc tgatggtgag 480  
actctgtttg gagccctta tgactttaga tatggtctag ctgctgaagg tcacccttca 540  
caagtgggtt ccaagtccct caaagatcta aagaatttga tagaagaagc aagcaattcc 600  
aataatggga agccagtgat acttctctcc cacagtttag gaggcctatt tgcctacaa 660  
ctactaaata gaaaccccc ctcttggcgc aaaaaattca tcaaactt cattgctctt 720  
tcagctccat ggggtggtgc tatagacgaa atgtacacct ttgcatctgg caacactttg 780  
ggagtgcctc tagtggacct tttattagtg agggatgaac aaagaagctc cgagagtaac 840  
ctttggcttt tgcctaacc caaaaattttt ggtcctcaaa aaccaatagt gataactcca 900  
attaggcctt attcagctca tgacatggtt gattttctaa aagacattgg ttttcctgaa 960  
ggggtttatc cttatgaaac acgaattcta cccttgatag ggaacataaa agcaccacaa 1020  
gtgcctataa cttgtattat ggggaacggga gtgggaacct tggaaacatt gttttatggg 1080  
aaagggtgatt ttgatgaacg gccagaaata tcatatgggg atggtgatgg aacgggtgaac 1140  
ttggtgagct tggtggcgct tcaatcacta tggaaagagg agaaaaatca ataccttaaa 1200  
gtggttaaga tagatgggt gtctcacta tcaatactta aggatgaagt tgcactaaat 1260  
gaaatagtag gtgagattac ttcaattaat tctcatgctg agctcgggtt aagtaatttg 1320  
ttttcggggt aa 1332

<210> 14  
<211> 443  
<212> PRT  
<213> Glycine max

<400> 14  
Met Lys Lys Glu Gln Glu Glu Gly Leu Lys Ile Glu Val Ala Thr Leu  
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Thr Val Thr Val Val Val Val Met Leu Ser Leu Leu Cys Thr Cys Gly  
20 25 30  
Ala Ser Asn Leu Asp Pro Leu Ile Leu Ile Pro Gly Asn Gly Gly Asn  
35 40 45  
Gln Leu Glu Ala Arg Leu Thr Asn Gln Tyr Lys Pro Ser Thr Phe Ile  
50 55 60  
Cys Glu Ser Trp Tyr Pro Leu Ile Lys Lys Lys Asn Gly Trp Phe Arg  
65 70 75 80  
Leu Trp Phe Asp Ser Ser Val Ile Leu Ala Pro Phe Thr Gln Cys Phe  
85 90 95  
Ala Glu Arg Met Thr Leu His Tyr His Gln Glu Leu Asp Asp Tyr Phe  
100 105 110

Asn Thr Pro Gly Val Glu Thr Arg Val Pro His Phe Gly Ser Thr Asn  
 115 120 125  
 Ser Leu Leu Tyr Leu Asn Pro Arg Leu Lys His Ile Thr Gly Tyr Met  
 130 135 140  
 Ala Pro Leu Val Asp Ser Leu Gln Lys Leu Gly Tyr Ala Asp Gly Glu  
 145 150 155 160  
 Thr Leu Phe Gly Ala Pro Tyr Asp Phe Arg Tyr Gly Leu Ala Ala Glu  
 165 170 175  
 Gly His Pro Ser Gln Val Gly Ser Lys Phe Leu Lys Asp Leu Lys Asn  
 180 185 190  
 Leu Ile Glu Glu Ala Ser Asn Ser Asn Asn Gly Lys Pro Val Ile Leu  
 195 200 205  
 Leu Ser His Ser Leu Gly Gly Leu Phe Val Leu Gln Leu Leu Asn Arg  
 210 215 220  
 Asn Pro Pro Ser Trp Arg Lys Lys Phe Ile Lys His Phe Ile Ala Leu  
 225 230 235 240  
 Ser Ala Pro Trp Gly Gly Ala Ile Asp Glu Met Tyr Thr Phe Ala Ser  
 245 250 255  
 Gly Asn Thr Leu Gly Val Pro Leu Val Asp Pro Leu Leu Val Arg Asp  
 260 265 270  
 Glu Gln Arg Ser Ser Glu Ser Asn Leu Trp Leu Leu Pro Asn Pro Lys  
 275 280 285  
 Ile Phe Gly Pro Gln Lys Pro Ile Val Ile Thr Pro Ile Arg Pro Tyr  
 290 295 300  
 Ser Ala His Asp Met Val Asp Phe Leu Lys Asp Ile Gly Phe Pro Glu  
 305 310 315 320  
 Gly Val Tyr Pro Tyr Glu Thr Arg Ile Leu Pro Leu Ile Gly Asn Ile  
 325 330 335  
 Lys Ala Pro Gln Val Pro Ile Thr Cys Ile Met Gly Thr Gly Val Gly  
 340 345 350  
 Thr Leu Glu Thr Leu Phe Tyr Gly Lys Gly Asp Phe Asp Glu Arg Pro  
 355 360 365  
 Glu Ile Ser Tyr Gly Asp Gly Asp Gly Thr Val Asn Leu Val Ser Leu  
 370 375 380  
 Leu Ala Leu Gln Ser Leu Trp Lys Glu Glu Lys Asn Gln Tyr Leu Lys  
 385 390 395 400  
 Val Val Lys Ile Asp Gly Val Ser His Thr Ser Ile Leu Lys Asp Glu  
 405 410 415  
 Val Ala Leu Asn Glu Ile Val Gly Glu Ile Thr Ser Ile Asn Ser His  
 420 425 430

Ala Glu Leu Gly Leu Ser Asn Leu Phe Ser Gly  
 435 440

<210> 15  
 <211> 432  
 <212> PRT  
 <213> Arabidopsis thaliana

<400> 15  
 Met Lys Lys Ile Ser Ser His Tyr Ser Val Val Ile Ala Ile Leu Val  
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Val Val Thr Met Thr Ser Met Cys Gln Ala Val Gly Ser Asn Val Tyr  
 20 25 30

Pro Leu Ile Leu Val Pro Gly Asn Gly Gly Asn Gln Leu Glu Val Arg  
 35 40 45

Leu Asp Arg Glu Tyr Lys Pro Ser Ser Val Trp Cys Ser Ser Trp Leu  
 50 55 60

Tyr Pro Ile His Lys Lys Ser Gly Gly Trp Phe Arg Leu Trp Phe Asp  
 65 70 75 80

Ala Ala Val Leu Leu Ser Pro Phe Thr Arg Cys Phe Ser Asp Arg Met  
 85 90 95

Met Leu Tyr Tyr Asp Pro Asp Leu Asp Asp Tyr Gln Asn Ala Pro Gly  
 100 105 110

Val Gln Thr Arg Val Pro His Phe Gly Ser Thr Lys Ser Leu Leu Tyr  
 115 120 125

Leu Asp Pro Arg Leu Arg Asp Ala Thr Ser Tyr Met Glu His Leu Val  
 130 135 140

Lys Ala Leu Glu Lys Lys Cys Gly Tyr Val Asn Asp Gln Thr Ile Leu  
 145 150 155 160

Gly Ala Pro Tyr Asp Phe Arg Tyr Gly Leu Ala Ala Ser Gly His Pro  
 165 170 175

Ser Arg Val Ala Ser Gln Phe Leu Gln Asp Leu Lys Gln Leu Val Glu  
 180 185 190

Lys Thr Ser Ser Glu Asn Glu Gly Lys Pro Val Ile Leu Leu Ser His  
 195 200 205

Ser Leu Gly Gly Leu Phe Val Leu His Phe Leu Asn Arg Thr Thr Pro  
 210 215 220

Ser Trp Arg Arg Lys Tyr Ile Lys His Phe Val Ala Leu Ala Ala Pro  
 225 230 235 240

Trp Gly Gly Thr Ile Ser Gln Met Lys Thr Phe Ala Ser Gly Asn Thr  
 245 250 255

Leu Gly Val Pro Leu Val Asn Pro Leu Leu Val Arg Arg His Gln Arg  
 260 265 270

Thr Ser Glu Ser Asn Gln Trp Leu Leu Pro Ser Thr Lys Val Phe His  
 275 280 285  
 Asp Arg Thr Lys Pro Leu Val Val Thr Pro Gln Val Asn Tyr Thr Ala  
 290 295 300  
 Tyr Glu Met Asp Arg Phe Phe Ala Asp Ile Gly Phe Ser Gln Gly Val  
 305 310 315 320  
 Val Pro Tyr Lys Thr Arg Val Leu Pro Leu Thr Glu Glu Leu Met Thr  
 325 330 335  
 Pro Gly Val Pro Val Thr Cys Ile Tyr Gly Arg Gly Val Asp Thr Pro  
 340 345 350  
 Glu Val Leu Met Tyr Gly Lys Gly Gly Phe Asp Lys Gln Pro Glu Ile  
 355 360 365  
 Lys Tyr Gly Asp Gly Asp Gly Thr Val Asn Leu Ala Ser Leu Ala Ala  
 370 375 380  
 Leu Lys Val Asp Ser Leu Asn Thr Val Glu Ile Asp Gly Val Ser His  
 385 390 395 400  
 Thr Ser Ile Leu Lys Asp Glu Ile Ala Leu Lys Glu Ile Met Lys Gln  
 405 410 415  
 Ile Ser Ile Ile Asn Tyr Glu Leu Ala Asn Val Asn Ala Val Asn Glu  
 420 425 430